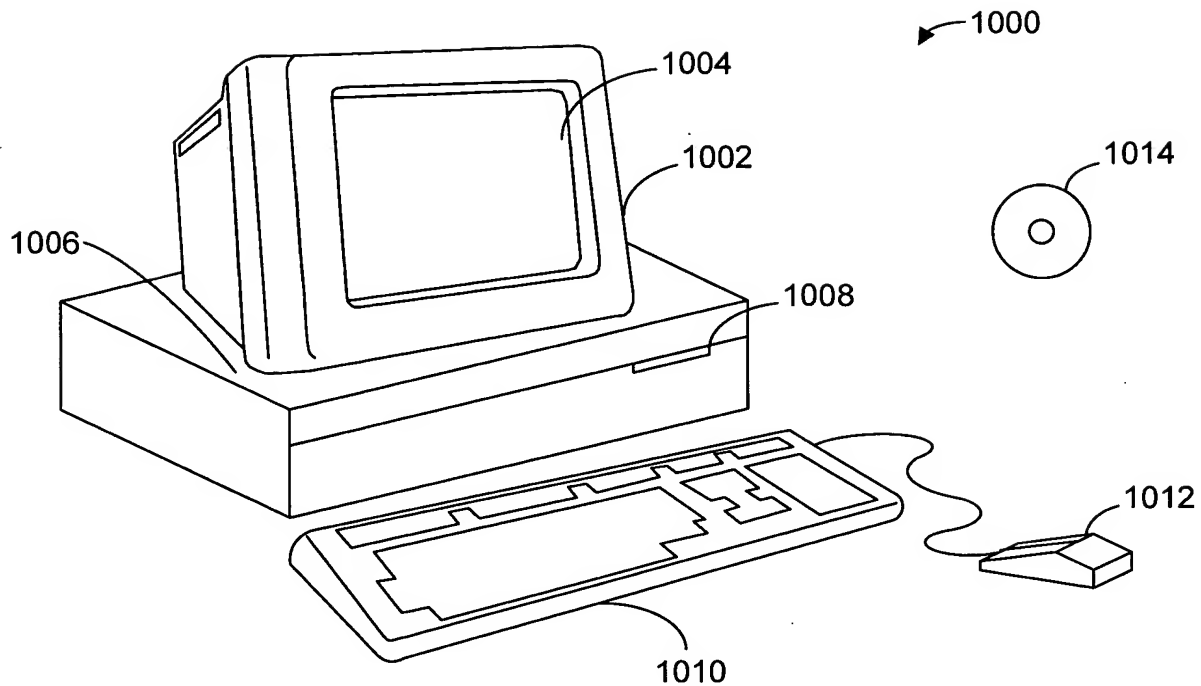


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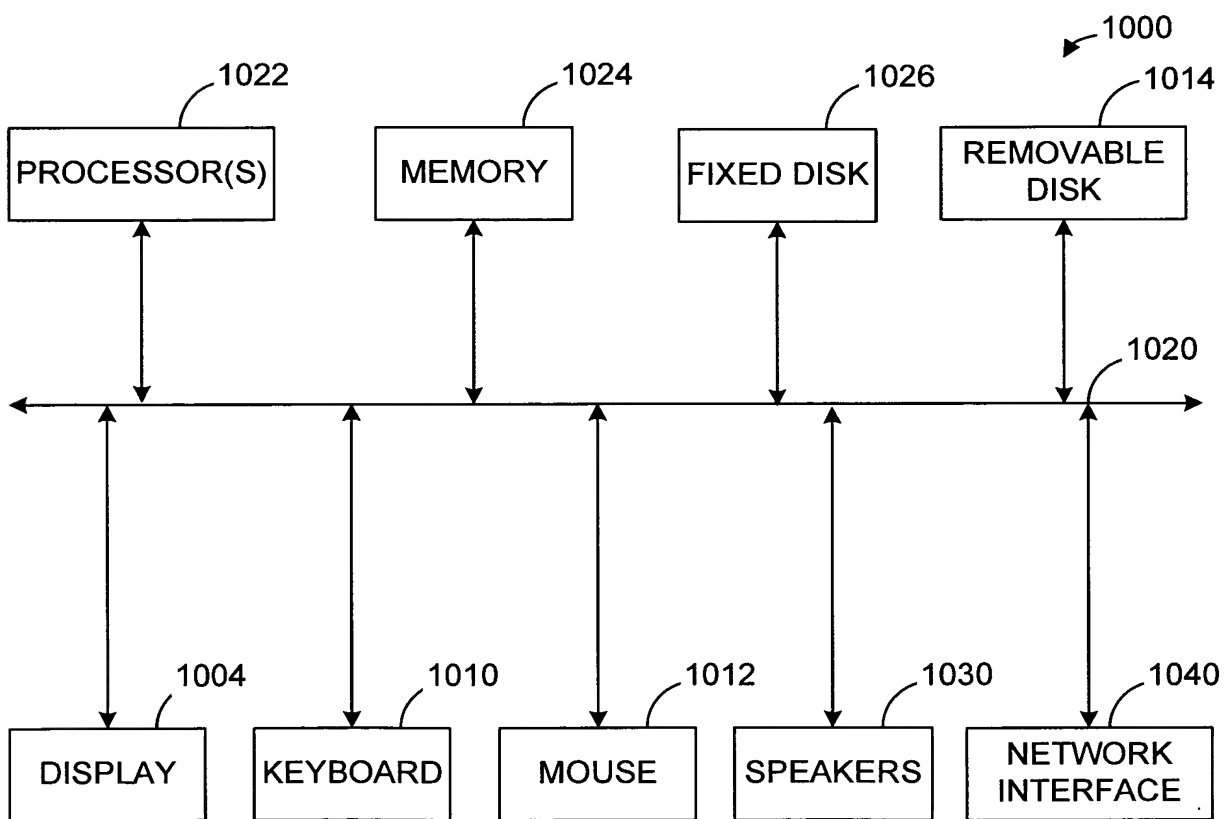
**FIG. 1A**

	A	B
1	Dependence of power on QTL allele frequency	
2	QTL frequency	0.05
3	Broad-sense heritability	=Baseline!B3
4	Dominance effect	=Baseline!B4
5	tail area: controls	=Baseline!B5
6	tail area: cases	=Baseline!B6
7	Marker frequency	0.05
8	D'	=Baseline!B8
9	Cases	=Baseline!B9
10	Controls per case	=Baseline!B10
11	Type I error rate	=Baseline!B11
12	Additive effect	=SQRT((B3/(1-B3))/(2*B2*(1-B2)*((1-B4*(2*B2-1))^2 + 2*B2*(1-B2)*B4^2)))
13	Trait max for controls	-1.28262403179506
14	Trait min for cases	0.0881695648961275
32	Population attributable risk	= 1 - B26 / (B28*B2^2 + B27*2*B2*(1-B2) + B26*(1-B2)^2)
33	Genotype relative risk	= B27/B26
34	Allele frequency in controls	= B7 + B8 * (B23-B2) * MIN((1-B7)/(1-B2), B7/B2)
35	Allele frequency in cases	= B7 + B8 * (B24-B2) * MIN((1-B7)/(1-B2), B7/B2)
36	Power to detect QTL	=NORMSDIST(SQRT( 2*B9*(B35-B34)^2 / ((1+1/B10)*B25*(1-B25))) ) - B31)

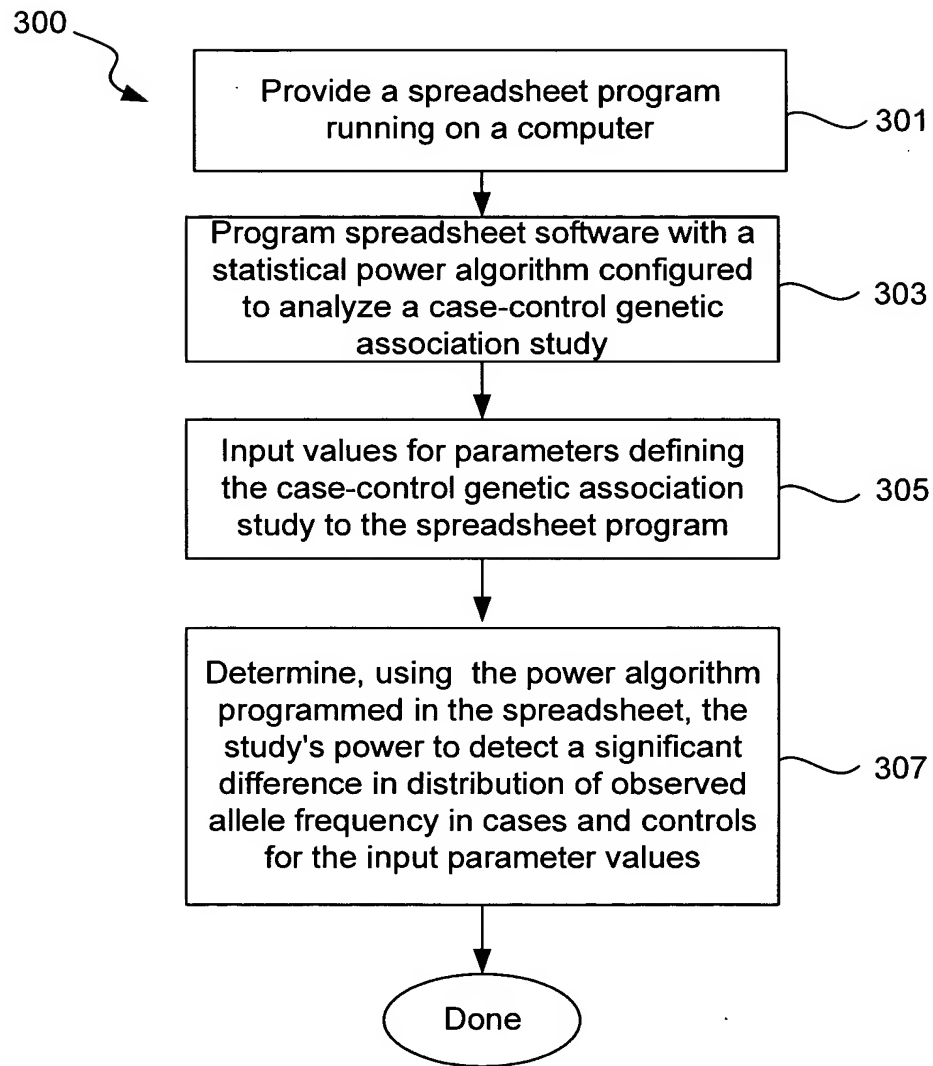
**FIG. 1B**



**FIG. 2A**



**FIG. 2B**



**FIG. 3**

**Baseline model parameters:**

<b>QTL frequency, p</b>	<b>0.20</b>
<b>Broad-sense heritability</b>	<b>0.040</b>
<b>Dominance effect, d/a</b>	<b>0</b>
<b>tail area: controls</b>	<b>25.0%</b>
<b>tail area: cases</b>	<b>25.0%</b>
<b>Marker frequency, s</b>	<b>0.20</b>
<b>D'</b>	<b>1</b>
<b>Cases</b>	<b>240</b>
<b>Controls per case</b>	<b>1.0</b>
<b>Type I error rate</b>	<b>5.0E-08</b>

***FIG. 4A***

Dependence of power on QTL allele frequency

QTL frequency	0.05	0.10	0.15	0.20	0.25	0.50	0.75	0.80	0.85	0.90	0.95
Broad-sense heritability	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040
Dominance effect	0	0	0	0	0	0	0	0	0	0	0
tail area: controls	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%
tail area: cases	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%
Marker frequency	0.05	0.10	0.15	0.20	0.25	0.50	0.75	0.80	0.85	0.90	0.95
D'	1	1	1	1	1	1	124	1	1	1	1
Cases	240	240	240	240	240	240	0	240	240	240	240
Controls per case	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Type I error rate	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08
Additive effect	0.662	0.481	0.404	0.361	0.333	0.289	0.333	0.361	0.404	0.481	0.662
Trait max for controls	-1.283	-1.075	-0.972	-0.906	-0.856	-0.688	-0.520	-0.470	-0.403	-0.300	-0.088
Trait min for cases	0.088	0.300	0.403	0.470	0.520	0.688	0.856	0.906	0.972	1.075	1.283
Population attributable risk	0.095	0.132	0.162	0.189	0.214	0.343	0.531	0.589	0.663	0.760	0.897
Genotype relative risk	2.052	1.758	1.637	1.572	1.533	1.495	1.673	1.778	1.962	2.359	3.855
Allele frequency in controls	0.019	0.053	0.092	0.133	0.176	0.410	0.668	0.723	0.780	0.840	0.905
Allele frequency in cases	0.095	0.160	0.220	0.277	0.332	0.590	0.824	0.867	0.908	0.947	0.981
Power to detect QTL	0.356	0.463	0.504	0.524	0.537	0.554	0.537	0.524	0.504	0.463	0.356

FIG. 4B

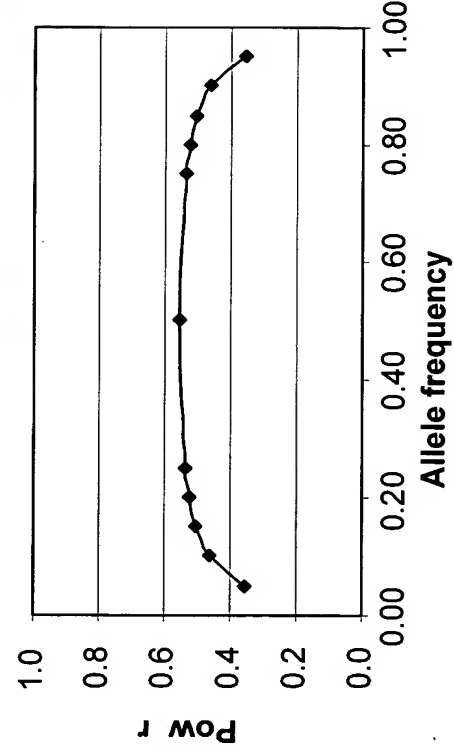


FIG. 4C

# Dependence of power on QTL effect size

QTL frequency	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
Broad-sense heritability	0.010	0.015	0.020	0.025	0.030	0.035	0.040	0.045	0.050	0.050
Dominance effect	0	0	0	0	0	0	0	0	0	0
tail area: controls	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%
tail area: cases	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%
Marker frequency	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
D'	1	1	1	1	1	1	1	1	1	1
Cases	240	240	240	240	240	240	240	240	240	240
Controls per case	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Type I error rate	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08
Additive effect, a	0.178	0.218	0.253	0.283	0.311	0.337	0.361	0.384	0.406	0.406
Trait max for controls	-0.785	-0.809	-0.833	-0.853	-0.869	-0.886	-0.903	-0.918	-0.933	-0.933
Trait min for cases	0.570	0.548	0.529	0.512	0.497	0.483	0.470	0.458	0.446	0.446
Population attributable risk	0.092	0.113	0.132	0.148	0.162	0.176	0.189	0.201	0.213	0.213
Genotype relative risk	1.251	1.316	1.373	1.427	1.477	1.525	1.572	1.618	1.662	1.662
Allele frequency in controls	0.165	0.158	0.152	0.146	0.142	0.137	0.133	0.130	0.126	0.126
Allele frequency in cases	0.237	0.246	0.253	0.260	0.266	0.272	0.277	0.282	0.287	0.287
Power to detect QTL	0.004	0.020	0.063	0.141	0.252	0.385	0.523	0.650	0.756	0.756

FIG. 5A

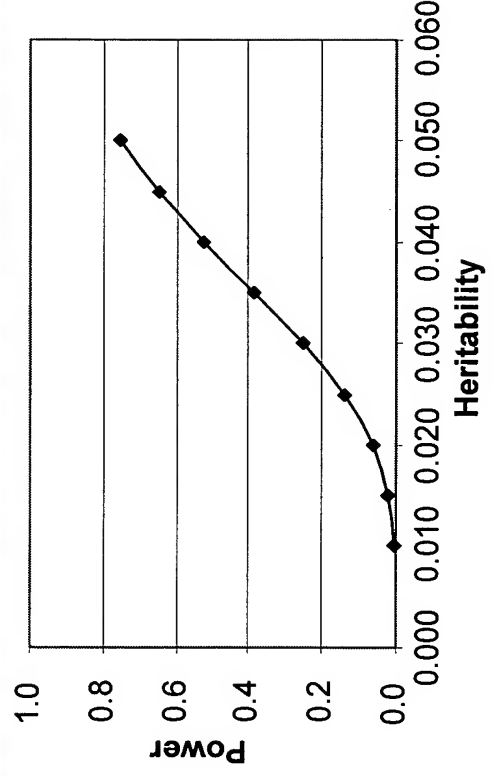


FIG. 5B

# Dependence of power on QTL mode of action

QTL frequency	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
Broad- sense heritability	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040	0.040
Dominance effect	-1	-0.75	-0.5	-0.25	0	0.25	0.5	0.75	1			
tail area: controls	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%
tail area: cases	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%	25.0%
Marker frequency	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20	0.20
D'	1	1	1	1	1	1	1	1	1	1	1	1
Cases	240	240	240	240	240	240	240	240	240	240	240	240
Controls per case	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Type I error rate	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08	5.0E-08
Additive effect	0.521	0.519	0.478	0.419	0.361	0.311	0.271	0.239	0.213			
Trait max for controls	-1.345	-1.308	-1.246	-1.175	-1.116	-1.069	-1.033	-1.004	-0.981			
Trait min for cases	0.515	0.552	0.616	0.684	0.739	0.788	0.829	0.856	0.880			
Population attributable risk	0.086	0.144	0.186	0.211	0.223	0.228	0.231	0.232	0.232			
Genotype relative risk	1.000	1.220	1.433	1.593	1.695	1.759	1.799	1.822	1.838			
Allele frequency in controls	0.172	0.153	0.139	0.130	0.127	0.125	0.125	0.126	0.127			
Allele frequency in cases	0.269	0.285	0.292	0.294	0.292	0.289	0.287	0.284	0.282			
Power to detect QTL	0.033	0.305	0.635	0.769	0.798	0.790	0.767	0.733	0.699			

FIG. 6A

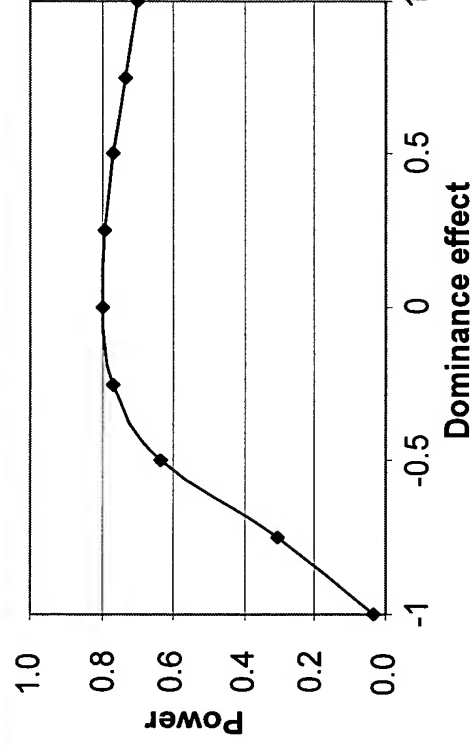
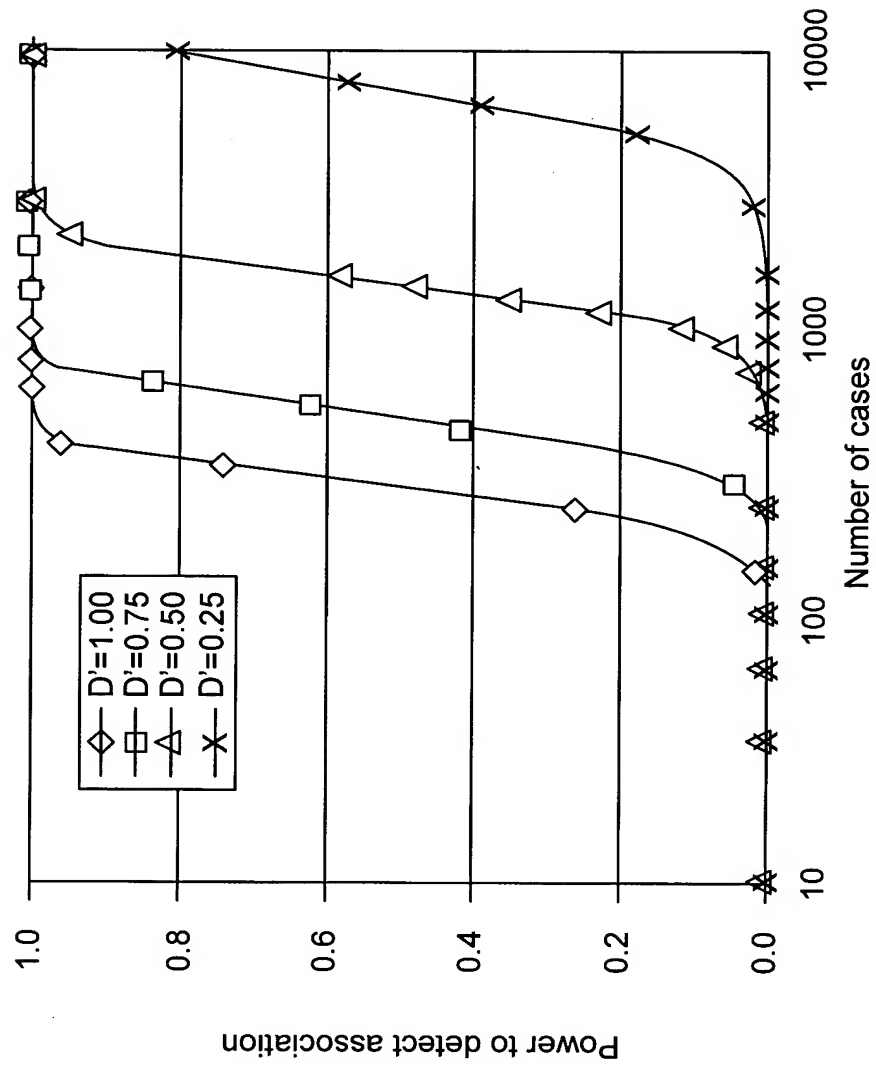


FIG. 6B





**FIG. 7**